

GenCore version 5.1.6
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ON protein - Protein search, using sw model

Run on: September 29, 2003, 13:56:00 ; Search time 26 Seconds

(Without alignments)

576.131 Million cell updates/sec

Title: US-09-818-143-22

Perfect score: 539

Sequence: 1 MEALANYNFPKSFREPEDA.....RLKVGRPQASQRKLKETGLC 99

Scoring table: Blosum62

Gapop 10.0 , Gapext 0.5

Searched: 566894 seqs, 151307093 residues

Total number of hits satisfying chosen parameters: 566894

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database :

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Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubpaas/US08_PUB...pep;*
3: /cgn2_6/ptodata/1/pubpaas/US08_PUB...pep;*
4: /cgn2_6/ptodata/1/pubpaas/US07_PUBCOMB.pep;*
5: /cgn2_6/ptodata/1/pubpaas/US07...NEW_PUB...pep;*
6: /cgn2_6/ptodata/1/pubpaas/US07_PUBCOMB.pep;*
7: /cgn2_6/ptodata/1/pubpaas/US08_PUBCOMB.pep;*
8: /cgn2_6/ptodata/1/pubpaas/US08_PUBCOMB.pep;*
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10: /cgn2_6/ptodata/1/pubpaas/US09_PUBCOMB.pep;*
11: /cgn2_6/ptodata/1/pubpaas/US09C_PUBCOMB.pep;*
12: /cgn2_6/ptodata/1/pubpaas/US09C...NEW_PUB...pep;*
13: /cgn2_6/ptodata/1/pubpaas/US10_PUBCOMB.pep;*
14: /cgn2_6/ptodata/1/pubpaas/US10_PUBCOMB.pep;*
15: /cgn2_6/ptodata/1/pubpaas/US10C_PUBCOMB.pep;*
16: /cgn2_6/ptodata/1/pubpaas/US10...NEW_PUB...pep;*
17: /cgn2_6/ptodata/1/pubpaas/US09...NEW_PUB...pep;*
18: /cgn2_6/ptodata/1/pubpaas/US09_PUBCOMB.pep;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	539	100.0	9 US-09-818-143-22	Sequence 22, Appi
2	539	100.0	99 10 US-09-974-298-149	Sequence 149, Appi
3	79.5	14.7	>322 9 US-09-789-136-6	Sequence 6, Appi
4	79.5	14.7	322 12 US-09-789-831-6	Sequence 5, Appi
5	79.5	14.7	345 9 US-09-789-836-5	Sequence 5, Appi
6	79.5	14.7	345 12 US-10-251-661-10	Sequence 10, Appi
7	79.5	14.7	345 15 US-10-060-036-183	Sequence 183, Appi
8	73.5	13.6	419 16 US-10-138-098-25	Sequence 25, Appi
9	70.5	13.1	419 16 US-10-138-098-25	Sequence 27, Appi
10	69.5	12.9	323 15 US-10-205-823-62	Sequence 27, Appi
11	69	12.8	323 15 US-10-177-293-33	Sequence 62, Appi
12	69	12.8	4123 15 US-10-213-509-5	Sequence 5, Appi
13	69	12.8	627 12 US-10-349-836-6	Sequence 6, Appi
14	67.5	12.5	597 9 US-09-853-386-93	Sequence 93, Appi
15	67	12.4		

Pred. No. 22

Length: 99

Other Information:

US-09-818-143-22

Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEALANYNFPKSFREPEDAKEYVRLKGRPQASQRKLKETGLC 99

Db 1 MEALANYNFPKSFREPEDAKEYVRLKGRPQASQRKLKETGLC 99

Qy 61 RACACHQNAQGAPKAMPVRLKGRPQASQRKLKETGLC 99

Db 61 RACACHQNAQGAPKAMPVRLKGRPQASQRKLKETGLC 99

Qy 1 MEALANYNFPKSFREPEDAKEYVRLKGRPQASQRKLKETGLC 99

Db 1 MEALANYNFPKSFREPEDAKEYVRLKGRPQASQRKLKETGLC 99

Qy 1 MEALANYNFPKSFREPEDAKEYVRLKGRPQASQRKLKETGLC 99

Db 1 MEALANYNFPKSFREPEDAKEYVRLKGRPQASQRKLKETGLC 99

RESULT 2

US-09-974-298-149

; Sequence 149, Application US/09974298

PATENT NO. US20020156263A1
 GENERAL INFORMATION:
 APPLICANT: Chen, Hwei-Mei
 TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
 FILE REFERENCE: PA-0037 P
 CURRENT APPLICATION NUMBER: US/09/974,298
 CURRENT FILING DATE: 2001-10-04
 PRIOR APPLICATION NUMBER: 60/238,331
 PRIOR FILING DATE: 2000-05-10
 NUMBER OF SEQ ID NOS: 194
 SOFTWARE: PERL Program
 SEQ ID NO: 149
 LENGTH: 99
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURES:
 NAME/KEY: misc-feature
 OTHER INFORMATION: Incyte ID No. US20020156263A1 1556751CD1
 us-09-974-298-149

Query Match 100.0%; Score 539; DB 10; Length 99;
 Best Local Similarity 100.0%; Pred. No. 4.e-18;
 Matches 99; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0; Gaps 5;
 Qy 1 MEALANVNPKEFRPEDAGESQGGCVPARAPQMTGPGCSSPGLQNFSPQRKEN 60
 Db 1 MEALANVNPKEFRPEDAGESQGGCVPARAPQMTGPGCSSPGLQNFSPQRKEN 60
 Qy 61 RACACWQNAGPARKNPVCYRLKVGPOASQRKLETLGLC 99
 Db 61 RACACWQNAGPARKNPVCYRLKVGPOASQRKLETLGLC 99
 SEQ ID NO: 3
 LENGTH: 99

Query Match 100.0%; Score 539; DB 10; Length 99;
 Best Local Similarity 100.0%; Pred. No. 4.e-18;
 Matches 99; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0; Gaps 5;
 Qy 1 MEALANVNPKEFRPEDAGESQGGCVPARAPQMTGPGCSSPGLQNFSPQRKEN 60
 Db 1 MEALANVNPKEFRPEDAGESQGGCVPARAPQMTGPGCSSPGLQNFSPQRKEN 60
 Qy 61 RACACWQNAGPARKNPVCYRLKVGPOASQRKLETLGLC 99
 Db 61 RACACWQNAGPARKNPVCYRLKVGPOASQRKLETLGLC 99
 SEQ ID NO: 3
 LENGTH: 99

Query Match 100.0%; Score 539; DB 10; Length 99;
 Best Local Similarity 100.0%; Pred. No. 4.e-18;
 Matches 99; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0; Gaps 5;
 Qy 1 MEALANVNPKEFRPEDAGESQGGCVPARAPQMTGPGCSSPGLQNFSPQRKEN 60
 Db 1 MEALANVNPKEFRPEDAGESQGGCVPARAPQMTGPGCSSPGLQNFSPQRKEN 60
 Qy 61 RACACWQNAGPARKNPVCYRLKVGPOASQRKLETLGLC 99
 Db 61 RACACWQNAGPARKNPVCYRLKVGPOASQRKLETLGLC 99
 SEQ ID NO: 3
 LENGTH: 99

Query Match 100.0%; Score 539; DB 10; Length 99;
 Best Local Similarity 100.0%; Pred. No. 4.e-18;
 Matches 99; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0; Gaps 5;

Query Match 100.0%; Score 539; DB 10; Length 99;
 Best Local Similarity 100.0%; Pred. No. 4.e-18;
 Matches 99; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0; Gaps 5;

Query Match 100.0%; Score 539; DB 10; Length 99;
 Best Local Similarity 100.0%; Pred. No. 4.e-18;
 Matches 99; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0; Gaps 5;

Query Match 100.0%; Score 539; DB 10; Length 99;
 Best Local Similarity 100.0%; Pred. No. 4.e-18;
 Matches 99; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0; Gaps 5;

Query Match 100.0%; Score 539; DB 10; Length 99;
 Best Local Similarity 100.0%; Pred. No. 4.e-18;
 Matches 99; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0; Gaps 5;

US-09-789-831-6
 Sequence 6, Application US/09789831
 Publication No. US2003016658A1
 GENERAL INFORMATION:
 APPLICANT: SEALY, LINDA
 TITLE OF INVENTION: C/EBP-BETA ISOFORMS AND METHODS OF USE IN CELL REGULATION
 FILE REFERENCE: N-6978
 CURRENT APPLICATION NUMBER: US/09/789,831
 CURRENT FILING DATE: 2001-02-20
 PRIORITY NUMBER: 60/183,532
 PRIORITY FILING DATE: 2000-02-18
 NUMBER OF SEQ ID NOS: 32
 PRIORITY APPLICATION NUMBER: 60/183,532
 PRIORITY FILING DATE: 2000-02-18
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 6
 LENGTH: 322
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-789-831-6
 Query Match 14.7%; Score 79.5; DB 12; Length 322;
 Best Local Similarity 26.2%; Pred. No. 2.5;
 Matches 32; Conservative 10; Mismatches 39; Indels 41; Gaps 5;
 Qy 10 PRKSFRPEDAGESQGGCVPARAPQMTGPGCSSPGLQNFSP 55
 Db 158 PADCKRKEEAGPGGAGMAAGFPYALRAYLGQAVPSGSGLSTSSSPGTP--SP 215
 Qy 56 QRKENRACACWQNAGPAP-----
 Db 216 ADAKAPPTACYAGPAPSOVSKRAKKTVDKHSDEYKIRERNNIAVR--KSRDKAKMRN 273
 Qy 93 LK 94
 Db 274 LE 275
 SEQ ID NO: 5
 LENGTH: 345
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-789-836-5
 Sequence 5, Application US/09789836
 Publication No. US20030082204A1
 GENERAL INFORMATION:
 APPLICANT: BRIGHAM, KENNETH L.
 APPLICANT: STOECENKO, ARLENE A.
 APPLICANT: BRIGHAM, KENNETH L.
 APPLICANT: SEALEY, LINDA
 TITLE OF INVENTION: TREATMENT OF INFLAMMATION WITH P20
 FILE REFERENCE: N-6977
 CURRENT APPLICATION NUMBER: US/09/789,836
 CURRENT FILING DATE: 2001-02-20
 PRIORITY NUMBER: 60/183,584
 PRIORITY FILING DATE: 2000-02-18
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 6
 LENGTH: 322
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-789-836-6
 Query Match 14.7%; Score 79.5; DB 9; Length 322;
 Best Local Similarity 26.2%; Pred. No. 2.5;
 Matches 32; Conservative 10; Mismatches 39; Indels 41; Gaps 5;
 Qy 10 PRKSFRPEDAGESQGGCVPARAPQMTGPGCSSPGLQNFSP 55
 Db 158 PADCKRKEEAGPGGAGMAAGFPYALRAYLGQAVPSGSGLSTSSSPGTP--SP 215
 Qy 56 QRKENRACACWQNAGPAP-----
 Db 216 ADAKAPPTACYAGPAPSOVSKRAKKTVDKHSDEYKIRERNNIAVR--KSRDKAKMRN 273
 Qy 93 LK 94
 Db 274 LE 275
 SEQ ID NO: 5
 LENGTH: 345
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-789-836-5
 Query Match 14.7%; Score 79.5; DB 9; Length 345;
 Best Local Similarity 26.2%; Pred. No. 2.7;
 Matches 32; Conservative 10; Mismatches 39; Indels 41; Gaps 5;
 Qy 10 PRKSFRPEDAGESQGGCVPARAPQMTGPGCSSPGLQNFSP 55
 Db 181 PADCKRKEEAGPGGAGMAAGFPYALRAYLGQAVPSGSGLSTSSSPGTP--SP 238
 Qy 56 QRKENRACACWQNAGPAP-----
 Db 239 ADAKAPPTACYAGPAPSOVSKRAKKTVDKHSDEYKIRERNNIAVR--KSRDKAKMRN 296
 Qy 93 LK 94
 Db 274 LE 275
 SEQ ID NO: 4

NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32747
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32747

Query Match 14 28; Score 76.5; DB 4; Length 253;
Best Local Similarity 31.3%; Pred. No. 0.34%;
Matches 26; Mismatches 6; Indels 25; Gaps 6;

Qy 10 PRKS-FRPEDAGKESGSGGFCYPALARPTMV-----TGPCCSSPGQLNFNSPQRK 58
Db 12 PRNAWWRPEAA---GGAGASATPGCRPRTYRCATGRTATSSSPRCAP-----PVRC 61

Qy 59 ENRACACHONAGP---APKNCMC 78
Db 62 KPAACACMSAHAPTYCPR-PRC 83

RESULT 3
US-09-252-991A-23683
Sequence 23683, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: US 60/094,788
; PRIOR FILING DATE: 1998-07-27
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23683
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23683

Query Match 13 8%; Score 74.5; DB 4; Length 138;
Best Local Similarity 29.9%; Pred. No. 0.27%;
Matches 26; Conservate 7; Mismatches 31; Indels 23; Gaps 5;

Qy 10 PRKS-FRPEDAGKESGSGGFCYPALARPTMV-----TGPCCSSPGQLNFNSPQRK 67
b 70 PRKRCP-----SSQ-----PRKRSRATPAIGPSCSGTSLASMP-----SCWN 109

Qy 68 NAG-PARKNPMCYRLKVGGRQASOKRL 93
Db 110 SSSPRASPAVRAATTNPWRSRSL 136

RESULT 4
US-09-252-991A-31845
Sequence 31845, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31845
; LENGTH: 298

Query Match 13 8%; Score 74.5; DB 4; Length 298;
Best Local Similarity 27.8%; Pred. No. 0.72%;
Matches 22; Conservate 9; Mismatches 25; Indels 23; Gaps 4;

Qy 10 PRKS-FRPEDAGKESGSGGFCYPALARPTMV-----TGPCCSSPGQLNFNSPQRK 62
Db 1 PPRQWTPRDSRWA-RNGATPTPSTSPTSPRSAP----PPTRTRARAATAWKPS 54

Qy 63 -----CHQNONGPARK 74
Db 55 PAASPRTCACWR--PAPR 70

RESULT 5
US-09-252-991A-19223
Sequence 19223, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19223
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19223

Query Match 13 7%; Score 74; DB 4; Length 176;
Best Local Similarity 25.7%; Pred. No. 0.43%;
Matches 21; Conservate 17; Mismatches 39; Indels 22; Gaps 5;

Qy 11 RKSFRPEDAGKESGSGGFCYP-----ARQDQHMTGPGCSSP-GLONNSPORKERA 62
Db 34 RRSRSRNADR---QRAWHHPAPVPRAREQAAARRACSPQTDRAPRLOPPA 89

Qy 63 C-----ACQNAGAPKKNPMCYRLKVG----RPAQSOKRLKETG 97
Db 90 CAPYAVDARRASAPTHRRPAPVRPGAGSPPGNRQAVSRGG 134

RESULT 6
US-09-252-991A-29859
Sequence 29859, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29859
; LENGTH: 683
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29859

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Om protein - protein search, using sw model

Run on: September 29, 2003, 13:55:22 ; Search time 96 Seconds
(without alignments)
266.117 Million cell updates/sec

Title: US-09-818-143-22

Perfect score: 539

Sequence: 1 MEALANYNPFKSFPEAG.....RLKVGRPQASQRKLRETGLC 99

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5
Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summariesDatabase : SPTREMBL_23:
1: sp_archae:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp Rodent:*

12: sp_virus:*

13: sp_vertbrate:*

14: spUnclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

ALIGNMENTS

RESULT 1
Q9UFS0 PRELIMINARY; PRT; 99 AA.
ID Q9UFS0; PRELIMINARY;
AC OGUSPO; PRT; 99 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Hypothetical Protein (DKZ2P434N161 protein).
GN DKZ2P434N161.
OS Homo sapiens (Human). Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Mammalia; Primates; Catarrhini; Hominidae; Homo.
NCB_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RN TISSUE=Testis;
RN Submitted (SPP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RN TISSUE=Uterus;
RN Submitted (SPP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	539	100.0	99	4	Q9UFS0	Q9UFS0 homo sapien
2	86.5	16.0	557	3	Q9UFS4	Q9UFS4 schizosaccharomyces pombe
3	83.5	15.5	1196	5	Q8T433	Q8T433 drosophila
4	78	14.5	504	5	Q8SP12	Q8SP12 drosophila
5	78	14.5	504	5	Q8MY8	Q8MY8 drosophila
6	76.5	14.2	208	13	Q93592	Q93592 astyanax fuscus
7	75.5	14.0	1534	5	Q9VPH3	Q9VPH3 drosophila
8	75	13.9	712	4	Q8NCN4	Q8NCN4 homo sapien
9	74.5	13.8	268	4	Q96884	Q96884 homo sapien
10	73.5	13.6	345	4	Q96FH2	Q96FH2 homo sapien
11	73	13.5	386	10	Q832F1	Q832F1 oryza sativa
12	73	13.5	945	5	Q9NKT7	Q9NKT7 leishmania
13	73	13.5	2087	5	Q8AXL2	Q8AXL2 leishmania
14	72.5	13.5	323	4	Q8TB94	Q8TB94 homo sapien
15	72.5	13.5	504	5	P90730	P90730 ceratitis cerasivae
16	72	13.4	2533	5	P90589	P90589 paramecium caudatum

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OM protein - protein search, using sw model

Run on: September 29, 2003, 13:55:21 ; Search time 23 Seconds
(without alignments)
202,419 Million cell updates/sec

Title: US-09-818-143-22
Perfect score: 539
Sequence: 1 MEALANYNFPKSFPRPEDAG.....RLKVRPQASORKLKETGLC 99

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	79.5	14.7	345	1	CEBB_HUMAN	P17676 homo sapien
2	79.5	14.7	998	1	RRPO_BOV	Q99220 bovinus vi
3	78.5	14.6	998	1	RRPO_FHV	Q56929 flock house
4	78	14.5	504	1	C6A9_DROME	Q22594 drosophila
5	78	14.5	504	1	C6A1_DRONE	Q39774 drosophila
6	78	14.5	825	1	SE5_RAT	Q30030 ratus norv
7	77	14.3	348	1	CEBB_BOVIN	Q27555 bos taurus
8	75.5	14.0	998	1	RRPO_BIV	Q96631 black beetle
9	75	13.9	305	1	GSH2_MOUSE	P31316 mus musculus
10	74	13.7	119	1	VTC3_DROME	Q65211 drosophila
11	72	13.4	137	1	VIT_STREU	P96151 strongyloice
12	72	13.4	740	1	POB_MAIZE	P57118 zea mays (m
13	70	13.0	2003	1	NTC1_HUMAN	Q99466 homo sapien
14	69.5	12.9	506	1	C6A1_DROME	P33270 drosophila
15	69	12.8	323	1	CG96_HUMAN	Q3y3a4 homo sapien
16	69	12.8	569	1	SIL1_MOUSE	Q29933 mus musculus
17	68	12.6	433	1	F0T4_RAT	Q29944 ratus norv
18	68	12.6	3726	1	ABP1_MOUSE	Q00519 mus musculus
19	67.5	12.5	627	1	ACH4_HUMAN	P33681 homo sapien
20	67	12.4	597	1	NR41_RAT	P28292 ratus norv
21	67	12.4	1235	1	IRSL_RAT	P55570 ratus norv
22	66.5	12.3	935	1	Y95_ADP02	P03286 human adeno
23	66.5	12.3	506	1	C6A8_DROME	Q27593 drosophila
24	66.5	12.3	1335	1	XDH_MOUSE	Q00519 mus musculus
25	66	12.2	507	1	C6A1_DRONE	Q9vb31 drosophila
26	65.5	12.2	1786	1	UVRA_CHLUTR	Q84337 chlamydia t
27	65	12.1	172	1	CX42_RAT	Q9ly94 ratus norv
28	65	12.1	559	1	DACA_HUMAN	Q9byj9 homo sapien
29	65	12.1	606	1	E75_MEPE02	Q77245 metapenaeus
30	64.5	12.0	457	1	Z185_HUMAN	Q15231 homo sapien
31	64	11.9	907	1	GCP3_HUMAN	Q96cw5 homo sapien
32	64	11.9	3703	1	ABP1_HUMAN	Q15911 homo sapien
33	63.5	11.8	591	1	PAR4_HUMAN	Q96013 homo sapien

ALIGNMENTS

RESULT 1	CEBB_HUMAN	STANDARD:	PRT;	345 AA.
ID	CEBB_HUMAN			
AC	P17676; Q9H425;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	CCAVY/enhancer binding protein beta (C/EBP beta) (Nuclear factor NF-IL6) (transcription factor 5).			
DN	CCEBPB OR TCF5			
OS	Homo sapiens (Human).			
OC	Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TAXID=9606;			
[1]				
RN				
RP				
SEQUENCE FROM N.A.				
RC				
TISSUE=Placenta;				
RX				
MEDLINE=90269225; PubMed=2112087;				
RA				
Akira S., Isshiki H., Sugita T., Tanabe O., Kishimoto T.; "A nuclear factor for IL-6 expression (NF-IL6) is a member of a C/EBP family." J. Clin. Endocrinol. 1990; 130: 1897-1906.				
RA				
RA				
RT				
RT				
RT				
EMBO J. 9:1897-1906 (1990).				
[2]				
RN				
SEQUENCE FROM N.A.				
RX				
MEDLINE=21638749; PubMed=11780052;				
RA				
Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavridis G., Mattheyses G., Babguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blahey S.E., Bridgeman A.M., Brown A.J., Buck D., Burill W.D., Butler A.P., Carder C., Clark N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Cleee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cory B., Dunn M.R., Ellington A., Coville G.J., Deadman R., Dhami P.D., Dunn M.R., Ellington J., Frankland J.A., Fraser A., French L., Garner P., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Hartley J.J., Heath P.D., Ho S., Holden J.L., Houlden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., King A.M., Leversha M.A., Lloyd C., Laird G.K., Lavori S., Lehvaseslahti M.H., Leversha M.A., Lovell J.D., Lovell D.M., Lovell J.D., March V.L., Martin S.L., McConnaehie L.J., McElroy K., McMurray A.A., Milne S.A., Misty D., Moore J.M., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillipinore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Stewart C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tronmans A.C., Vaudin M., Wallis J.M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Wilmung L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J., "The DNA sequence and comparative analysis of human chromosome 20." Nature 414:865-871(2001); "FUNCTION: IMPORTANT TRANSCRIPTIONAL ACTIVATOR IN THE REGULATION OF GENES INVOLVED IN IMMUNE AND INFLAMMATORY RESPONSES. SPECIFICALLY BINDS TO AN IL-1 RESPONSE ELEMENT IN THE IL-6 GENE. NF-IL6 ALSO				

Viruses; ssRNA positive-strand viruses, no DNA stage; Nodaviridae;
 OC Alphanoctaviridae
 OC NCBI_TaxID=12286;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21351093; PubMed=11457991;
 RA Johnson K.N., Johnson K.L., Dasgupta R., Gritsch T., Ball L.A.;
 RT "Comparisons among the larger genome segments of six nodaviruses and
 their encoded RNA replicases."
 RT J. Gen. Virol. 82:1855-1866(2001).
 RL 82:1855-1866(2001).
 CC -I- FUNCTION: Replicates the viral genome which is composed of two
 CC segments, RNA1 and RNA2.
 CC -I- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC (RNA) (N).
 CC -I- SIMILARITY: BELONGS TO THE NODAVIRUSES RNA POLYMERASE FAMILY.
 CC
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 CC or send an email to license@ebi.ac.uk.)
 CC
 DR EMBL; AF29080; AAK1751_1; "
 DR InterPro; IPR007095; RNA_P01_DS_PS.
 KW Transferase; RNA-directed RNA polymerase.
 SQ SEQUENCE 998 AA; 111203 MW; 7FAFFEEFC7329253 CRC64;
 DR
 Best Local Similarity 14.7%; Score 79.5; DB 1; Length 998;
 Matches 33; Conservative 12; Mismatches 31; Indels 41; Gaps 0.
 Qy 7 VNFRPKS --FRPEDA--GKESGS-----QGFCFY-----PAAPRQTH--VN
 Db 628 INCRAKKGKFRRYEPGMVGRSGSPPTPHNTQYNACTVEYALKFEPYDNPANPDLFLSL
 Qy 43 PSCCSGPQLQNFSPQRKENRACAGWAGAAPPKNCMVALKVRPQASQRKIKETG
 Db 688 PKCDDGLARATIQTKITNRAKCYG-----LELKV-----EKYNPEVGLC 7
 DR
 RRPQ_FHV STANDARD; PRT; 998 AA.
 ID RRPQ_FHV
 AC Q66529;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE RNA-directed RNA Polymerase (EC 2.7.7.48) (RdRp) (RNA replicase)
 DE (Protein A).
 OS Flock house virus (FHV).
 OX Viruses; ssRNA positive-strand viruses, no DNA stage; Nodaviridae;
 OX Alphanoctaviridae.
 NCBI_TaxID=12287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dasgupta R.;
 RT "Near identity in the polymerase gene of two serologically distinct
 nodaviruses."
 RT Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: Replicates the viral genome which is composed of two, R.
 CC segments, RNA1 and RNA2.
 CC -I- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC (RNA) (N).
 CC -I- SIMILARITY: BELONGS TO THE NODAVIRUSES RNA POLYMERASE FAMILY.
 CC
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 CC or send an email to license@ebi.ac.uk.)

Result No.	Query	Score	Match	Length	DB ID	Description
1	539	100.0	99	2	T17268	hypothetical prote
2	86.5	16.0	557	2	S14631	hypothetical prote
3	79.5	14.7	345	2	S12788	transcription fact
4	78.5	14.6	998	2	S41397	protein A -
5	78	14.5	825	2	JC4163	lock
6	75.5	14.0	998	1	QBBB1	DNA-binding prote
7	75	13.9	305	2	I57039	B1 protein - black
8	74	13.7	104	2	A22706	genomic screen hom
9	72	13.4	137	2	S00696	vitellogenin membra
10	72	13.4	2533	2	T03975	vitellogenin precu
11	72	13.4	2533	2	T28675	hypothetical prote
12	72	13.4	2533	2	T28677	alpha-51D immobili
13	71.5	13.3	401	2	T02830	hypothetical prote
14	70.5	13.1	3942	2	T42761	Bassoon protein -
15	69.5	12.9	507	1	A47198	cytochrome P450 6A
16	69.5	12.9	511	2	S24345	Balbiani ring 1 pr
17	68	12.6	751	2	F87789	protein C34G6.2 [1
18	67.5	12.5	98	2	F8304	hypothetical prote
19	67	12.5	627	2	JCA021	nicotinic acetylch
20	67	12.4	563	2	JQ0623	nerve growth facto
21	67	12.4	1235	1	S15948	insulin receptor S
22	66.5	12.3	75	2	S05989	Balbiani ring prot
23	66.5	12.3	95	2	A01858	hypothetical prote
24	66.5	12.3	294	2	S1341	cytochrome P450 mo
25	66.5	12.3	494	2	JCS320	hypothetical prote
26	66.5	12.3	906	2	T28034	xanthine dehydroge
27	66.5	12.3	1335	1	X03SDH	protein kinase (EC
28	66	12.2	108	2	S17199	protein W03A5.3 [1
29	66	12.2	457	2	E88456	Query Match

Copyright (c) 1993 - 2003 Campugen Ltd.	GenCore version 5.1.6	30	66	12.2	670	2	T49510
OM protein - protein search, using sw model		31	66	12.2	1101	2	T20881
Run on:	September 29, 2003, 13:55:22 ; Search time 40 Seconds (without alignments) 238.01 Million cell updates/sec	32	65.5	12.2	372	2	T286189
Title:	US-09-818-143-22	33	65.5	12.2	1786	1	H71527
Perfect score:	539	34	65	12.1	845	2	T17291
Sequence:	1 MEALANVNPPKSFREPDAG RLKVGRPQASQRILKETGLC 99	35	64.5	12.0	3938	2	T42761
Scoring table:	BLOSUM62	36	64	11.9	402	2	I46053
Searched:	Gapop 10.0 , Gapext 0.5	37	64	11.9	2783	1	A41948
Total number of hits satisfying chosen parameters:	283308	38	63.5	11.8	360	2	S75453
Minimum DB seq length: 0		39	63.5	11.8	596	2	F75302
Maximum DB seq length: 2000000000		40	63.5	11.8	649	2	S67787
Post-processing: Minimum Match 0%		41	63.5	11.8	736	2	T41259
Maximum Match 100%		42	63.5	11.8	813	2	T21192
Listing first 45 summaries		43	63	11.7	202	2	S20029
Database :	PIR76:*	44	63	11.7	303	2	T28999
	1: Pir1:*	45	63	11.7	390	1	W2WLRS
	2: Pir2:*						
	3: Pir3:*						
	4: pir4:*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
RESULT 1							
T17268							
hypothetical protein DKFZp434N161.1 - human							
C;Species: Homo sapiens (man)							
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999							
C;Accession: T17268							
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wleemann, S.							
submitted to the Protein Sequence Database, September 1999							
A;Reference number: 218723							
A;Accession: T17268							
A;Status: preliminary							
A;Molecule type: mRNA							
A;Cross-references: EMBL:AL117489							
A;Experimental source: adult testis; clone DKFZp434N161.1							
A;Note: DKFZp434N161.1							
Query Match	100.0%	Score	539;	DB 2;	Length	99;	
Best Local Similarity	100.0%	Pred. No.	2.6e-47;				
Matches	99;	Conservative	0;	Mismatches	0;	Indels	0;
Qy							
1 MEALANNEPKSERPEDAGKESSQQGFCYPAAQDQTMYTGPSSSPQLQNESPQRKEN' 60							
Db							
1 MEALANNEPKSERPEDAGKESSQQGFCYPAAQDQTMYTGPSSSPQLQNESPQRKEN' 60							
Qy							
61 RACACMONAGAPKNPCKYRLKVGRPQASQRKLKEKG LC 99							
Db							
61 RACACMONAGAPKNPCKYRLKVGRPQASQRKLKEKG LC 99							
RESULT 2							
T41631							
hypothetical protein SPCC830_05C - fission yeast (Schizosaccharomyces pombe)							
C;Species: Schizosaccharomyces pombe							
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999							
C;Accession: T41631							
R;McDouall, R.M.; Rajandream, M.A.; Barrell, B.G.; Ramsperger, U.; Pohl, T.							
submitted to the EMBL Data Library, August 1999							
A;Reference number: Z22005							
A;Accession: T41631							
A;Status: preliminary; translated from GB/EMBL/DDJB							
A;Molecule type: DNA							
A;Residues: 1-557 <CCD>							
A;Cross-references: EMBL:AL109850; PIDN:QAB52878_1; GSPDB:GN00068; SPDB:SPCC830_05C							
C;Genetics:							
A;Gene: SPDB:SPCC830_05C							
A;Map position: 3							
A;Intron: 56/3							
Query Match	16.0%	Score	86.5;	DB 2;	Length	557;	

Best Local Similarity 30.4%; Prod. No. 0.42; Mismatches 18; Indels 33; Gaps 6; Matches 28; Conservative 3; Species: Rattus norvegicus (Norway rat)

Qy 6 VNVPKRKSP--PDAEKES-GSOGGFCVPAARPQTAVT--GPSCSSP--GLONF----53 . Db 402 HTNYPDSFRNTLPTYSGKENKQSHNQLSIPSSPTBLSNDGPTSTPHSSLSNFNTCD 461

Qy 54 SPQRKENRACACWQNAPAPNPNMPCVRLKVRG 85 Db 462 SLFSNNNSLYGSTM-LHPRNPICVRQIGR 492

RESULT 5

JC163 DNA-binding protein 5E5 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 20-Jun-2000

C;Accession: JC4163; PC4040

R;Suzuki, E.; Kojima, N.; Yoshimura, K.; Obata, K.; Akayawa, K.

J. Biochem. 116, 122-126, 1995

A;Title: Cloning and sequence analysis of cDNA for a possible DNA-binding protein 5E5

A;Reference number: JC4163; MUID:96015159; PMID:8537300

A;Accession: JC4163

A;Molecule type: mRNA

A;Residues: 1-25 <Suz>

A;Cross references: DDBJ:D17934; NID:9531260; PIDN:BAA07153_1; PID:9531261

A;Experimental source: brain

A;Molecule type: protein

A;Residues: 230-455 <SPU2>

C;Comment: This protein has an abundance of arginine, a glycine-rich region and a proline-rich region at the C-terminal homologous domain.

C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homologous domain

C;Keywords: nerve; Phosphoprotein

F:436-443/Region: nuclear location signal

F:722-731/Region: proline cluster

F:62,258,345,360,404,413,570,613,653,752,820/Binding site: phosphate (Ser) (covalent)

Query Match Score 78; DB 2; Length 825; Best Local Similarity 30.3%; Pred. No. 4.3; Matches 27; Conservative 13; Mismatches 25; Indels 24; Gaps 4;

Qy 19 AGKRSGSQQGFCYPARPQMVITGSCSSPGLONFSPQRKNRACACW----68 Db 742 AGDGDASPGSRPARRPRLGFT-QRQPSP----FAEQEEGLRASPVCVDDGATAPDGDTA 796

Qy 69 ----AGPAPKNPVCVRLKVRGPOASQR 91 Db 797 SGVEPEAPSLSSTM---OMGRPPSK 822

RESULT 6

QBBBI

B1;protein - black beetle virus

C;Species: black beetle virus

C;Date: 30-Sep-1992 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

R;Dasgupta, R.

C;Accession: S78471; S28728; A23243 submitted to the EMBL Data Library, July 1986

A;Reference number: S78471

A;Molecule type: genomic RNA

A;Residues: 1-1998 <DAS>

A;Cross references: EMBL:X02196; NID:960679; PIDN:CAA26238_1; PID:960680

R;Dasgupta, R.

J. Mol. Biol. 182, 183-189, 1985

A;Title: Structure of the black beetle virus genome and its functional implications.

A;Reference number: S28728; MUID:85210903; PMID:839022

A;Molecule type: genomic RNA

A;Residues: 1-883 <DAW>

A;Cross references: EMBL:X02396

A;Accession: S28729

A;Molecule type: genomic RNA

A;Residues: 897-998 <DA2>

A;Cross references: EMBL:X02396

R;Giarino, L.A.; Ghosh, A.; Dasgupta, R.; Kaesberg, P.

Virology 139, 199-203, 1984

Best Local Similarity 14.6%; Prod. No. 4.6; Mismatches 10; Indels 32; Gaps 7; Matches 34; Conservative 10; Species: black beetle virus B1 protein

Qy 7 VNFPRKS---FRPE-DAGKESGS-----PAARPQTM---VGT 42

Qy 93 LK 94

b 297 LE 298

RESULT 4

S41397 Protein A - flock house virus

C;Species: flock house virus

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 11-Jan-2000

C;Accession: S41397

R;Dasgupta, R.

A;Description: Near identity in the polymerase gene of two serologically distinct nodavirus strains.

A;Reference number: S41397

A;Accession: S41397

A;Status: preliminary

A;Molecule type: genomic RNA

A;Residues: 1-998 <DAS>

A;Cross references: EMBL:X77156; NID:9450500; PIDN:CAA54399_1; PID:9450501

C;Superfamily: black beetle virus B1 protein

Query Match Score 78.5; DB 2; Length 998; Best Local Similarity 29.1%; Prod. No. 4.6; Mismatches 10; Indels 32; Gaps 7; Matches 34; Conservative 10; Species: black beetle virus B1 protein

Qy 93 LK 94

b 297 LE 298

RESULT 5

JC163 DNA-binding protein 5E5 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 20-Jun-2000

C;Accession: JC4163; PC4040

R;Suzuki, E.; Kojima, N.; Yoshimura, K.; Obata, K.; Akayawa, K.

J. Biochem. 116, 122-126, 1995

A;Title: Cloning and sequence analysis of cDNA for a possible DNA-binding protein 5E5

A;Reference number: JC4163; MUID:96015159; PMID:8537300

A;Accession: JC4163

A;Molecule type: mRNA

A;Residues: 1-25 <Suz>

A;Cross references: DDBJ:D17934; NID:9531260; PIDN:BAA07153_1; PID:9531261

A;Experimental source: brain

A;Molecule type: protein

A;Residues: 230-455 <SPU2>

C;Comment: This protein has an abundance of arginine, a glycine-rich region and a proline-rich region at the C-terminal homologous domain.

C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homologous domain

C;Keywords: nerve; Phosphoprotein

F:436-443/Region: nuclear location signal

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F:62,258,345,360,404,413,570,613,653,752,820/Binding site: phosphate (Ser) (covalent)

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Qy 19 AGKRSGSQQGFCYPARPQMVITGSCSSPGLONFSPQRKNRACACW----68 Db 742 AGDGDASPGSRPARRPRLGFT-QRQPSP----FAEQEEGLRASPVCVDDGATAPDGDTA 796

Qy 69 ----AGPAPKNPVCVRLKVRGPOASQR 91 Db 797 SGVEPEAPSLSSTM---OMGRPPSK 822

RESULT 6

QBBBI

B1;protein - black beetle virus

C;Species: black beetle virus

C;Date: 30-Sep-1992 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

R;Dasgupta, R.

C;Accession: S78471; S28728; A23243 submitted to the EMBL Data Library, July 1986

A;Reference number: S78471

A;Molecule type: genomic RNA

A;Residues: 1-1998 <DAS>

A;Cross references: EMBL:X02196; NID:960679; PIDN:CAA26238_1; PID:960680

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A;Reference number: S28728; MUID:85210903; PMID:839022

A;Molecule type: genomic RNA

A;Residues: 1-883 <DAW>

A;Cross references: EMBL:X02396

A;Accession: S28729

A;Molecule type: genomic RNA

A;Residues: 897-998 <DA2>

A;Cross references: EMBL:X02396

R;Giarino, L.A.; Ghosh, A.; Dasgupta, R.; Kaesberg, P.

Virology 139, 199-203, 1984